SEQUENCE LISTING


    (1) GENERAL INFORMATION

   (i) APPLICANT:   BILLING-MEDEL, PATRICIA A.
                  COHEN, MAURICE
                  COLPITTS, TRACEY L.
                  FRIEDMAN, PAULA N.
                  HAYDEN, MARK
                  KLASS, MICHAEL R.
                  ROBERTS-RAPP, LISA
                  RUSSELL, JOHN C.
                  STROUPE, STEPHEN D.




   (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
       FOR DETECTING DISEASES OF THE GASTROINTESTINAL
       TRACT

   (iii) NUMBER OF SEQUENCES: 25

   (iv) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE: Abbott Laboratories
    (B) STREET: 100 Abbott Park Road
    (C) CITY: Abbott Park
    (D) STATE: IL
    (E) COUNTRY: USA
    (F) ZIP: 60064-3500

   (v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Diskette
    (B) COMPUTER: IBM Compatible
    (C) OPERATING SYSTEM: DOS
    (D) SOFTWARE: FastSEQ for Windows Version 2.0

   (vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER:
    (B) FILING DATE:
    (C) CLASSIFICATION:

   (vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER: 08/828,845
    (B) FILING DATE: 31-MAR-1997


   (viii) ATTORNEY/AGENT INFORMATION:
    (A) NAME: Becker, Cheryl L.
    (B) REGISTRATION NUMBER: 35,441
    (C) REFERENCE/DOCKET NUMBER: 6066.US.P1

   (ix) TELECOMMUNICATION INFORMATION:
    (A) TELEPHONE: 847/935-1729
    (B) TELEFAX: 847/938-2623
    (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 254 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CTGGGATCAG CCACTGCAGC TCCCTGAGCA CTCTCTACAG AGACGCGGAC CCCAGACATG    60
AGGAGGCTCC TCCTGGTCAC CAGCCTGGTG GTTGTGCTGC TGTGGGAGGC AGGTGCAGTC   120
CCAGCACCCA AGGTCCCTAT CAAGATGCAA GTCAAACACT GGCCCTCAGA GCAGGACCCA   180
GAGAAGGCCT GGGGCGCCCG TGTGGTGGAG CCTCCGGAGA AGGACGACCA GCTGGTGGTG   240
CTGTTCCCTG TCCA                                                     254
```

    (2) INFORMATION FOR SEQ ID NO:2:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 261 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
AGCCACTGCA GCTCCCTGAG CACTCTCTAC AGAGACGCGG ACCCCAGACA TGAGGAGGCT    60
CCTCCTGGTC ACCAGCCTGG TGGTTGTGCT GCTGTGGGAG GCAGGTGCAG TCCCAGCACC   120
CAAGGTCCCT ATCAAGATGC AAGTCAAACA CTGGCCCTCA GAGCAGGACC CAGAGAAGGC   180
CTGGGGCGCC CGTGTGGTGG AGCCTCCGGA GAAGGACGAC CAGCTGGTGG TGCTGTTCCC   240
TGTCCAGAAG CCGAAACTCT T                                             261
```

    (2) INFORMATION FOR SEQ ID NO:3:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 534 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (ix) FEATURE:
    (A) NAME/KEY: base_polymorphism
    (B) LOCATION: 458
    (D) OTHER INFORMATION: /note= "'N' represents an A or G or
       T or C polymorphism at this position"


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
TCCCGGCCTG CTGGGGTTTA TTTGTCTAGC TGGGGCAGGG TAGGGAGGGT CCCAGTCCCA    60
ACAGCCTGGG CCTTGGGACA GGGCGGGGGC AGTGATGGCC CCTGGAGCCC TACTGGGGGT   120
GGTAGATGTG GTCTTGGTCT TCCTCCGGTC CCAGGAGCAC CTGGTGATTT GGCATCACCC   180
ACAACCGGGG CCTCTCCTCG CCCTGGTCCT CCTCAGGCGG AGGGTGGTAC AGGCTGTCAT   240
GGTCGGGCTC GGGACTCAGG ACACGGCCCA GGGTGTCCTC GGTCTCCATC CAGGCCTTGG   300
```

```
TGCCTGGAAG GATGGGGCCC CTGCCCTGAC CTCGTGGCTT CTCCTCGGTG GTCAAGAGTT    360
TCGGCTTCTG GACAGGGAAC AGCACCACCA GCTGGTCGTC CTTCTCCGGA GGCTCCACCA    420
CACGGGCGCC CCAGGCTTCT CTGGGTCCTG CTCTGAGNGG CAGTGTTTGA CTTGCATCTT    480
GATAGGGAAC TTGGGTGCTG GGAATGCACC TGCCTCCCAC AGAAGAAAAA CAAC          534
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 615 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
AGCCACTGCA GCTCCCTGAG CACTCTCTAC AGAGACGCGG ACCCCAGACA TGAGGAGGCT    60
CCTCCTGGTC ACCAGCCTGG TGGTTGTGCT GCTGTGGGAG GCAGGTGCAG TCCCAGCACC    120
CAAGGTCCCT ATCAAGATGC AAGTCAAACA CTGGCCCTCA GAGCAGGACC CAGAGAAGGC    180
CTGGGGCGCC CGTGTGGTGG AGCCTCCGGA GAAGGACGAC CAGCTGGTGG TGCTGTTCCC    240
TGTCCAGAAG CCGAAACTCT TGACCACCGA GGAGAAGCCA CGAGGTCAGG GCAGGGGCCC    300
CATCCTTCCA GGCACCAAGG CCTGGATGGA GACCGAGGAC ACCCTGGGCC GTGTCCTGAG    360
TCCCGAGCCC GACCATGACA GCCTGTACCA CCCTCCGCCT GAGGAGGACC AGGGCGAGGA    420
GAGGCCCCGG TTGTGGGTGA TGCCAAATCA CCAGGTGCTC CTGGGACCGG AGGAAGACCA    480
AGACCACATC TACCACCCCC AGTAGGGCTC CAGGGGCCAT CACTGCCCCC GCCCTGTCCC    540
AAGGCCCAGG CTGTTGGGAC TGGGACCCTC CCTACCCTGC CCCAGCTAGA CAAATAAACC    600
CCAGCAGGCC GGGCA                                                     615
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 622 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CTGGGATCAG CCACTGCAGC TCCCTGAGCA CTCTCTACAG AGACGCGGAC CCCAGACATG    60
AGGAGGCTCC TCCTGGTCAC CAGCCTGGTG GTTGTGCTGC TGTGGGAGGC AGGTGCAGTC    120
CCAGCACCCA AGGTCCCTAT CAAGATGCAA GTCAAACACT GGCCCTCAGA GCAGGACCCA    180
GAGAAGGCCT GGGGCGCCCG TGTGGTGGAG CCTCCGGAGA AGGACGACCA GCTGGTGGTG    240
CTGTTCCCTG TCCAGAAGCC GAAACTCTTG ACCACCGAGG AGAAGCCACG AGGTCAGGGC    300
AGGGGCCCCA TCCTTCCAGG CACCAAGGCC TGGATGGAGA CCGAGGACAC CCTGGGCCGT    360
GTCCTGAGTC CCGAGCCCGA CCATGACAGC CTGTACCACC CTCCGCCTGA GGAGGACCAG    420
GGCGAGGAGA GGCCCCGGTT GTGGGTGATG CCAAATCACC AGGTGCTCCT GGGACCGGAG    480
GAAGACCAAG ACCACATCTA CCACCCCCAG TAGGGCTCCA GGGGCCATCA CTGCCCCCGC    540
CCTGTCCCAA GGCCCAGGCT GTTGGGACTG GGACCCTCCC TACCCTGCCC CAGCTAGACA    600
AATAAACCCC AGCAGGCCGG GA                                             622
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 68 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single

(D) TOPOLOGY: linear


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC     60
CGGGAATT     68

    (2) INFORMATION FOR SEQ ID NO:7:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 68 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG     60
GAATTCCG     68

    (2) INFORMATION FOR SEQ ID NO:8:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 24 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCGGATAAC AATTTCACAC AGGA     24

    (2) INFORMATION FOR SEQ ID NO:9:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 18 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGTAAAACGA CGGCCAGT     18

    (2) INFORMATION FOR SEQ ID NO:10:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGTCCAGAA GCCGAAACTC                                                    20

      (2) INFORMATION FOR SEQ ID NO:11:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGAAGACCA AGACCACATC                                                    20

      (2) INFORMATION FOR SEQ ID NO:12:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 22 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTAGATGTG GTCTTGGTCT TC                                                 22

      (2) INFORMATION FOR SEQ ID NO:13:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 20 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCGGTGGTC AAGAGTTTCG                                                    20

      (2) INFORMATION FOR SEQ ID NO:14:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 24 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear


  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTCCCTGTCC AGAAGCCGAA ACTC                                               24

      (2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 25 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGGGTTTAT TTGTCTAGCT GGGGC                                    25

    (2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 151 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear


    (ii) MOLECULE TYPE: None


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu Trp
1               5                   10                  15
Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met Gln Val
            20                  25                  30
Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp Gly Ala Arg
        35                  40                  45
Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val Val Leu Phe Pro
    50                  55                  60
Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu Lys Pro Arg Gly Gln
65                  70                  75                      80
Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys Ala Trp Met Glu Thr Glu
            85                  90                  95
Asp Thr Leu Gly Arg Val Leu Ser Pro Glu Pro Asp His Asp Ser Leu
            100                 105                 110
Tyr His Pro Pro Pro Glu Glu Asp Gln Gly Glu Glu Arg Pro Arg Leu
        115                 120                 125
Trp Val Met Pro Asn His Gln Val Leu Leu Gly Pro Glu Glu Asp Gln
    130                 135                 140
Asp His Ile Tyr His Pro Gln
145                 150
```

    (2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 29 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met Gln Val Lys His
1               5                   10                  15
Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp Gly Ala
            20                  25
```

        (2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val Val Leu Phe
1               5                   10                  15
Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu Lys Pro Arg Gly
            20                  25                  30
Gln Gly Arg Gly
            35
```

        (2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Leu Pro Gly Thr Lys Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg
1               5                   10                  15
Val Leu Ser Pro Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro
            20                  25                  30
Glu Glu Asp
            35
```

        (2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Pro Glu Glu Asp Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro
1               5                   10                  15
```

Asn His Gln Val Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr
            20                    25                      30


        (2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 8 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp Tyr Lys Asp Asp Asp Asp Lys
 1               5


        (2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
 1               5                    10                      15
His His His His His
            20


        (2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 249 base pairs
        (B) TYPE: DNA
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATCAGCCA CTGCAGCTCC CTGAGCACTC TCTACAGAGA CGCGGACCCC AGACATGAGG    60
AGGCTCCTCC TGGTCACCAG CCTGGTGGTT GTGCTGCTGT GGGAGGCAGG TGCAGTCCCA   120
GCACCCAAGG TCCCTATCAA GATGCAAGTC AAACACTGGC CCTCAGAGCA GGACCCAGAG   180
AAGGCCTGGG GCGCCCGTGT GGTGGAGCCT CCGGAGAAGG ACGACCAGCT GGTGGTGCTG   240
TTCCCTGTC                                                           249


        (2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 336 base pairs
        (B) TYPE: DNA

```
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

GGCAGGTGCA GTCCCAGCAC CCAAGGTCCC TATCAAGATG CAAGTCAAAC ACTGGCCCTC     60
AGAGCAGGAC CCAGAGAAGG CCTGGGGCGC CCGTGTGGTG GAGCCTCCGG AGAAGGACGA    120
CCAGCTGGTG GTGCTGTTCC CTGTCCAGAA GCCGAAACTC TTGACCACCG AGGAGAAGCC    180
ACGAGGTCAG GGCAGGGGCC CCATCCTTCC AGGCACCAAG GCCTGGATGG AGACCGAGGA    240
CACCCTGGGC CGTGTCCTGA GTCCCGAGCC CGACCATGAC AGCCTGTACC ACCCTCCGCC    300
TGAGGAGGAC CAGGGCGAGG AGAGGCCCCG GTTGTG                             336
```

```
    (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 300 base pairs
    (B) TYPE: DNA
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ix)    FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 8
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
             T or C polymorphism at this position"

(ix)    FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 102
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
             T or C polymorphism at this position"

(ix)    FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 194
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
             T or C polymorphism at this position"

(ix)    FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 212
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
             T or C polymorphism at this position"

(ix)    FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 225
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
             T or C polymorphism at this position"

(ix)    FEATURE:
        (A) NAME/KEY: base_polymorphism
        (B) LOCATION: 230
        (D) OTHER INFORMATION: /note= "'N' represents an A or G or
             T or C polymorphism at this position"
```

```
(ix)   FEATURE:
       (A)  NAME/KEY: base_polymorphism
       (B)  LOCATION: 259
       (D)  OTHER INFORMATION: /note= "'N' represents an A or G or
            T or C polymorphism at this position"


(xi)  SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCCCCATNCT TCCAGGCACC AAGGCCTGGA TGGAGACCGA GGACACCCTG GGCCGTGTCC      60
TGAGTCCCGA GCCCGACCAT GACAGCCTGT ACCACCCTCC GNCTGAGGAG GACCAGGGCG     120
AGGAGAGGCC CCGGTTGTGG GTGATGCCAA ATCACCAGGT GCTCCTGGGA CCGGAGGAAG     180
ACCAAGACCA CATNTACCAA CCCCAGTAGG GNTTCAGGGG CCATNAGTGN CCCCGGCCTG     240
TTCCAAGGCC CAGGTGTTNG GATTGGACCT TCCTAACCTG CCCAGTTAGA CAAATAAAAC     300
```